IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: He et al. Attorney Docket No.: PF140C2

Application Serial No.: Unassigned Art Unit: Unassigned
Filed: Herewith Examiner: Unassigned

Title: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease-3 and 4

SUBMISSION OF SUBSTITUTE/FORMAL DRAWINGS

Commissioner for Patents Washington, D.C. 20231

Sir:

Please substitute the attached <u>7</u> sheets of formal drawings depicting Figures <u>1A-B, 2A-B, and 3A-C</u> for the corresponding drawings of Figures 1-3 originally filed with the application. Included herewith, as required under 37 C.F.R. § 1.121(a)(3)(ii), is a copy of the figures as originally filed with changes marked. Acknowledgement of the receipt, approval, and entry of these formal drawings into the above captioned application is respectfully requested.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted.

Dated: July 2,200/

Jonathan L. Klein (Reg. No. 41,119) Attorney for Applicants

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ILK/LT/ba

1/7 FIGURE 1A

1	GCACGAGAAACTTTGCTGTGCGCGTTCTCCCGCGCGCGCG	00
61	GGCCAACTTGGCAGAGCGCCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT	120
.21	GCGGGACACGGGTCGCTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCCGAGCCAG	180
81	GGGCGGTGCAAGCCCCGGCCCTACCCAGGGCGGCTCCTCCCTC	240
41	CTTTTAGTTTCGCTTATCGCTAAAGGGGCCCCAGACCCTTGCTGCGGAGCGACGGAGAGAG	300
01	$\begin{tabular}{lllllllllllllllllllllllllllllllllll$	360 8
61	TTGAAGAGCAGGGGTTGAGGATTCAGCAAATGAAGATTCAGTGGATGCTAAGCCAGACC	420
9	E E Q G V E D S A N E D S V D A K P D R	28
21	GGTCCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAAATGTCACCATGCGATCCA S S F V P S L F S K K K K N V T M R S I	480 48
29	SSFVPSLFSKKKKNVTMRSI	40
	TCAAGACCACCCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTGG	540
81		68
49	K T T R D R V P T Y Q Y N M N F E K L G	00
	GCAAATGCATCATAATAAACAACAAGAACTTTGATAAAGTGACAGGTATGGGCGTTCGAA	600
41		88
69	KCIIINNKNFDKVTGMGVRN	-
01	ACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTTGACG	660
89	G T D K D A E A L F K C F R S L G F D V	108
61	TGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCTG	720
.09	I V Y N D C S C A K M Q D L L K K A S E	128
21	AAGAGGACCATACAAATGCCGCCTGCTTCGCCTGCATCCTCTTAAGCCATGGAGAAGAAA	780
.29	EDHTNAACFACILLSHGEEN	148
.29		
81	ATGTAATTTATGGGAAAGATGGTGTCACACCAATAAAGGATTTGACAGCCCACTTTAGGG	840
49	VIYGKDGVTPIKDLTAHFRG	168
41	GGGATAGATGCAAAACCCTTTTAGAGAAACCCAAACTCTTCTTCATTCA	900
.69	DRCKTLLEKPKLFFIQACRG	188
		960
01	GGACCGAGCTTGATGATGCCATCCAGGCCGACCTGGGGCCCATCAATGACACAGATGCTA T R L D D A I O A D S G P I N D T D A N	208
.89	TELDDAIQADSGPINDTDAN	200

2/7 FIGURE 1B

ATCC	TCG	ATA	CAA	GAT	ccc	AGI	GGA	AGC	TGA	CTI	CCI	CTI	CGC	CTA		CAC	GGT	TCC		102
P	R	Y	K	I	P	V	E	A	D	F	L	F	Α	Y	s	T	V	P	G	228
GCTA	TTA	CTC	GTG	GAG	GAG	CCC	AGG	AAC	AGG	CTC	CTC	GTI	TGT	'GC#	AGC	CCI	CTG	CTC	CA	108
Y	Y	s	W	R	s	P	G	R	G	s	W	F	v	Q	A	L	С	s	I	248
TCCT	GGA	GGA	GCA	CGG	AAA	AGA	CCI	GGA	AAT	CAT	GCA	GAT	CCI	CAC	CAC	GGT	GAA	TGA	CA	114
T.	E	E	н	G	к	D	L	E	I	M	Q	Ι	L	T	R	V	N	D	R	268
_	_	_																		
GAGT	TGC	CAG	GCA	CTI	TGP	GTC	TCA	GTC	TGA	TGI	CCC	ACA	CTT	CCF	TGP	GAP	GAA	GCA	GA	120
v	A	R	H	F	Е	s	0	s	D	D	P	H	F	H	Ε	K	K	Q	1	288
TCCC	CTC	TGI	GGT	CTC	CAT	GCT	CAC	CAP	GGA	ACT	CTF	CTI	CAC	TC	ATA	GCC	ATA	TCA	.GG	120
P	С	v	v	s	М	L	T	K	E	L	Y	F	s	Q						30:
GGTA	CAI	TCI	AGC	TGP	GAP	GCF	ATO	GGT	CAC	TCI	TT	ATO	CAA	CAC	ATT	TT	TTP	TGC	TC	132
TTGA	CAA	ATT	CAG	AAA	TTC	TCC	AGG	ATI	TTP	AT:	TCF	GGA	AAA	TGT	CTAC	: 1	369			
	P GCTA Y TCCT L GAGT V TCCCC P GGTA	PR GCTATTA YY TCCTGGA LE GAGTTGC VA TCCCCTG PC	PRY GCTATTACTC YYS TCCTGGAGGA LEEE GAGTTGCAG TCCCCTGTGT PCV GGTACATTCT	PRYK GCTATTACTCGTG YYSW TCCTGGAGGAGCA LEEH GAGTTGCCAGGCA VAR TCCCCTGTGTGGT PCVV GGTACATTCTAGC	PRYKI GCTATTACTCGTGGAG YYSWR TCCTGGAGGAGCACCC LEEHG GAGTTGCCAGGCACTT VARHF TCCCCTGTGTGGTCTC PCVVS GGTACATTCTAGCTGA	PRYKIP GCTATTACTCGTGGAGGAG YYSWRS TCCTGGAGGAGCACGGAAA LEEHGK GAGTTGCCAGGCACTTTGAVARHFE VARHFE TCCCCTGTGTGTGTCTCCAT PCVVSM	PRYKIPV GCTATTACTCGTGGAGGAGCCC YYSWRSP TCCTGGAGGAGCACGGAAAAAGA LEFEHGKD GAGTTGCCAGGCACTTTGAGTC VARHFES TCCCCTGTGTGGTCTCCATGCT PCVVSML GGTACATTCTAGCTGAGAACCA	PRYKIPVE GCTATTACTCGTGGAGGAGCCCAGG YYSWRSPG TCCTGGAGGAGCACGGAAAAGACCI LEEHGKDL GAGTTGCCAGGCACTTTGAGTCTCA VARHFESQ TCCCCTGTGGGTCTCCATGCTCAC PCVVSMLT GGTACATTCTAGCTGAGAACAATC	PRYKIPVEA GCTATTACTCGTGGAGGAGCCCAGGAAC YYSWRSPGR TCCTGGAGGAGCACGGAAAAGACCTGGA LEEHGKDLE GAGTTGCCAGGCACTTGAGTCTCAGTC VARHFESQS TCCCCTGTGTGGTCTCATGCTCACCAA PCVVSMLTX GGTACATTCTAGCTGAGAAGACTTAGAGAAGACTTAGCTGAGAGAATGGGT	PRYKIPVEAD GCTATTACTCGTGGAGGAGCCCAGGAAGAGGYYSWRSPGRG TCCTGGAGGAGCACGGAAAAGACCTGGAAAT LEEHGKKDLEI GAGTTGCCAGGACTTTGAGTCTCAGTCTGAVAR VARHFESOSSON TCCCCTGTGTGGTCTCCATGCTCACCAAGGA PCVVSMLTTKE	PRYKIPVE A DF GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTT YYSWRSPGRGACCTGGAAAGAGCCTGAAAATCAT LEEBHGKDLEIM GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATCT VARHFESQSSDDD TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACC PCVVSMLTKEL GGTACATTCTAGCTGAGAAGCAATGGTCACCTA	PRYKIPVE A DFL GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTC YYSWRSPGRGG TCCTGGAGGAGCACGGAAAAGACTCTGGAAATCATCCC LEEHGKDLEIMQ GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCC VARHFESQSACTTTGAGTCTCAGTCTGATGACCC VARHFESQSACTTTGAGTCTCACCAAGGAACCTE PCVVSMLTVSMLTVSGTCACCAAGGAACCTE PCVVSMLTVSMLTVSGTCACTCATTG	PRYKIPVE A DFL F GCTATTACTCGTGGAGGAGCCCCAGGAAGAGGCTCCTGGTT YYSWRSPGRGC TCCTGGAGGAGCACGGAAAAGACTCTGGAAATCATCCAGAT LEEHGKDLEIWQI GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCAC VARHFESQUSDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	PRYKIPVE A DFLFA GCTATTACTCGTGGAGGAGGCCCAGGAAGAGGGCTCCTGGTTTGT YYSWRSPGRGSSWFV TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCT LEEHGKDLEIMQIL GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCACACTT VARHFESQSODPHFF TCCCCTGTGGGGTCTCCCATGCTCACCAAGGAACCTACTTCAC PCVVSMLTX	PRYKIPVE A DFLFAY GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAYYSWRSFGRACCTGGAAATCATGCAGATCCTCAC LEEBGK DLEIMQILT GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCAYARHFESQVARHFESQVSDPFHFH TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCACTTACTCAGTCCPCVARHFESQVSDPFHFH TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCTACTTCAGTCCPCVVSNNLTTAGGATCCTCATCAGTCAGCAAGGAACTCTACTTCAGTCAG	PRYKIPVE A DFLFAYS GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAAGC YYSWRSPGRG CTATTACTCGTGGAGAAGGCCCCAGGAAGAGGCTCCTGGTTTGTGCAAGC YSWRSPGRG CTATTACTCGTGAGGACCCGAAAAGAACCTGGAAATCATTGCAGGATCCTCACCAC LEEBHGKDLEIMQILTR GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGA VARHFESQSSDDDPHFHE TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCTACTTCAGTCAATA PCVVSMLTX	PRYKIPVE A DFLFAYST GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTCCAAGCCCT YYSWRSPGRGG LEEHGKDLEELGAAAGACTGGAAATCATCCAGATCCTCACCAGGGT LEEHGKDLEELGAAAGACTGGAAATCATCCAGAATCCTCACCAGGGT LEEHGKDLEIMQILTRRV GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAA VARHFESQSDPFHHEK TCCCCTGTGTGGTCTCCATCCTCACCAAGGAACTCTACTTCAGTCAATAGCC PCVVSMLTKELY	PRYKIPVE A DFLFAYSTV GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTOTGCAAGCCCTCTG YYSWRSPGRGS TCCTGGAGGAGCACGGAAAAGACTGGAAATCATCACGAGTCCTCACCAGGGTGAA LEEHGKDLEINQILTRV GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACTTCCATGAGAAGA VARHFESQSDPHFHEKK TCCCCTGTGTGGTCTCCATCCTCACCAAGGAACTCTACTTCAGTCAATAGCCATA PCVVSMLTKELY	PRYKIPVE A DFLFAYSTVP GCTATTACTCGTGGAGGAGCCCAGGAAGAGGGCTCCTGGTTTGTGCAAGCCCTCTGCTC YYSWRSPGRAG TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATGA LEFHGKDLFINA LEFHGKDLFINA GAGTTGCCAGGCACTTTGAGTCCAGTCTGATGACCCACACTTCCATGAGAAGAAGCC VARHFESQSDDPHFHEKKQ TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCACTTCAGTCAATAGCCATATCA PCVVSMLTT GGGTACATTCTAGCTCACCAAGGAACTCTACTTCAGTCAATAGCCATATCA PCVVSMLTT GGGTACATTCTAGCTGAGAAGGAATGGGTCACTCAGTTAATGAATCACATTTTTTTATGC	GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAAGCCCTCTGCTCCA Y Y S W R S P G R G S W F V Q A L C S I TCCTGGAGGACCACGGAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATAGCA L E E H G K D L E I M Q I L T R V N D R CACTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGGAAG

3/7 FIGURE 2A

1	GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGC	CAG 60	
61	CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCC	CAG 120	o
121	GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTCGGTGGGTG	GCC 180	٥
181	CTGCACCTGCCTCTTCCCGCATTCTCATTAATAAAGGTATCCATGGAGAACACTGAA) M E N T E	AAC 240 N 6)
241 7	L TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACATGGAAGCGAAC / S V D S K S I K N L E P K I I H G S E	ICA 300 S 26)
301	ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGT	TTA 360 L 46)
361 47	TGTATAATAATTAATAAGAATTTTCATAAAGCACTGGAATGACATCTCGGTCTC	GGT 420 G 66	Э
421 67	L ACAGATGTCGATGCAGCAAACCTCAGGGAAACATTCAGAAACTTGAAATATGAAGTC/	AGG 480 R 86	0
481 87	L AATAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAA 7 N K N D L T R E E I V E L M R D V S K	GAA 540 E 106	
	GATCACAGCAAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGAAGAA		
107		I 126	
601 127	1 ATTTTTGGAACAAATGGACCTGTTGACCTGAAAAAAATAACAAACTTTTTCAGAGGG 7 I F G T N G P V D L K K I T N F F R G	D 146	
661 147	L CGTTGTAGAAGTCTAACTGGAAAACCCAAACTTTTCATTATTCAGGCCTGCCGTGGT 7 R C R S L T G K P K L F I I Q A C R G	ACA 720 T 166	
721 167	GAACTGGACTGTGCATTGAGACAGACAGTGGTGTTGATGATGACATGGCGTGTCAT; 7 E L D C G I E T D S G V D D D M A C H	AAA 780 K 186	
781 187	1 ATACCAGTGGAGGCCGACTTCTTGTATGCATACTCCACAGCACCTGGTTATTATTCT. 7 I P V E A D F L Y A Y S T A P G Y Y S	IGG 840 W 200	

4/7 FIGURE 2B

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841	CCN	ת ה ה	ጥሮ ኔ	220	СЪТ	GGC	TCC	TGG	ттс	ATC	CAG	TCG	CTI	rTGT	GCC	ATO	CTO	AAA	CAG	TAT	900
	00.0	MWI		K	D	G	S	w	F	т	0	S	т.	C	Δ	м	т.	к	O	Y	226
207	R	N	s	K	D	G	5	**	E	-	~	2		_	n	**		• • • • • • • • • • • • • • • • • • • •	×	-	
														•			•			•	
901	GCC	GAC	AAG	CTT	GAA	TTT	ATG	CAC	ATI	CTT	ACC	CGG	GTT	CAAC	CCGF	AAA	GTO	GCF	ACA	GAA	960
227	Δ	D	ĸ	т.	E	F	м	н	T	L	T	R	v	N	R	K	v	A	T	E	246
221	25	_	1	-	~	-	•••														
				•			•			•				· · .					- n ma		1020
961	TTT	GAG	TCC	TTT	TCC	TTT	GAC	GCT	ACT	TTT											
247	F	E	s	F	S	F	D	Α	T	F	Η	A	K	K	Q	I	P	С	Ι	٧	266
	TCC					C 3 3	cmc	m z m	mma	ייי איייי	CAC	מביחי	aci	ימממ	reen	יייה	ידידי	GTO	GTT	TTT	1080
1021								.141		V V	H	*	1101								277
267	S	М	L	T	K	Е	L	Y	F	Y	н	^									211
1081	TTT.	AGT	ጥጥር	TAT	GCC	AAG	TGA	GAA	GAT	GGT	AT	TTT	rgg	GTAC	TG	CATI	TCC	CTC	TCF	TTG	1140
1001																					
				•																	
1141	GGG	ACC	TAC	TCT	CAI	GCT	'G 1	.159	,												

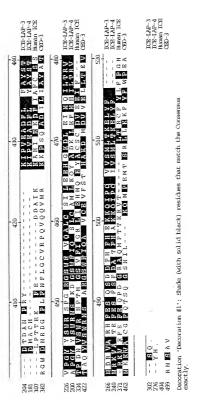
FIGURE 3A

1	10	- 20	30	- 07
	MADD Q		GCIBBOG NSVDSKS TINGLEDEFLOTR KVDEITBVIIAK	M E D ICE-LAP-3 I K M ICE-LAP-4 V H Huwan ICE V I M CED-3
	- 05	- 83	- 22	L 88-
92	SAMEDSWDA,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	K P D R S S F	ICE-LAP-3
8 3	KEEMEKUKRENATVM SDNGDMINS-CGTVR	MDKTRALIDS REKRREIVKA	WORRGDVA TDAF	Human ICE DAL CED-3
	- 86	100	011	120
81	₩ 0	KNWTMRS		ICE-IAP-3
3 63 P	RSTGHEGLAEVLEPL	GAQACQIC ARS M DSNA	TYIC VEFECPMSPASHRI	Human ICE tsra CED-3
	130	140	150	160
9 8	KTTRDR	R V P T		ICE-LAP-3
38 71	- EEDSVLAGTLG LSPAGYTSPINRVHRD	- LSADQTSG SVSSFF	NY	Human ICE SRSRCED-3
	170	180	190	200
88			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ICE-LAP-3
8 2	-INMODSQGV	SSENTANDAV INAMPSOPSS	Q DN P = F ANSSFTGCSSLG	r s s s cno-3

FIGURE 3B

ICE-LAP-3 ICE-LAP-4 Human ICE CED-3	ICE-LAP-3 ICE-LAP-4 Hunan ICE CED-3	ICE-LAP-3 ICE-LAP-4 Human ICE CED-3	TCE-LAP-3 ICE-LAP-4 Human ICE CED-3	ICE-LAP-3 ICE-LAP-4 Human ICE
240 2 K S A E I E T T - M	280 OKDAEAL DVDAANE	320 DHT NAA HKTS D(S ESHGDS	360 TAHFRGD TON FFRGO FUMINTK YDL INAA	400 N D
230 EEAQRIWK PTISRVFD	270 M G V R N G T I M T S R S G T I P R R T G A E	310 KKASEB RDVSKR EAPAHRPE RDFAKH	E M M M	390 DAIQADGGPIN CGIETDSGVDD SPGVVWFKDSVG
220 	260 NKWPDKVTG NKNPHKSTG NEFPDS NEFPDS	CSCAKMODFE TRRETVEEN TASDMYTE TRGRGMILLTI	- DG - V - NG - P SEQVP - DDIP	380 G T E L I G T E L I
210 YQV SGSYK BGPTQVIFH	250 250 2 G KC I I I N 5 G R T R L A L I I G 8 G P R G M C L I I I N	290 V I V Y N D C Y E V V I V Y E V K N K N T V Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	330 H G E E N V I V H G I R E G I C H G E B E O I I	370 PKLFETOACE PKLFTIOACE
R R R R R R R R R R R R R R R R R R R		FKCFRSLG RETFRUTK TMLEONLG	CPACITES SFVCVLLS TFL-VFMS AIL-VILS	RCKTLLEK RCRELTGK NCPSIKDK

FIGURE 3C



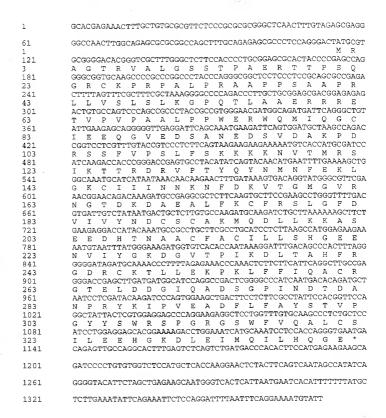


Figure 1

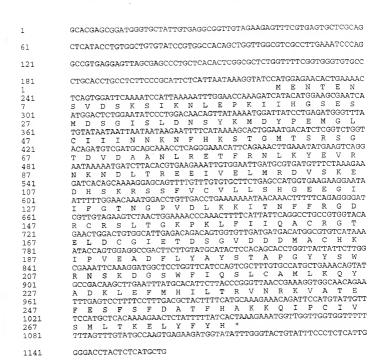


Figure 2

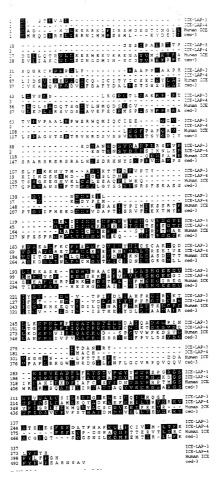


Figure 3